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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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model
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using
search,
protein
1
protein
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4, 2005, 12:11:19; Search time 41 Seconds (without alignments) 624.236 Million cell updates/sec January Run on:

US-10-006-867-2 1392 1 MWWPQQGLSFLPSALVIWTS......xDTAPCPINNERTRLLSRDI 266 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	hypothetical prote		S.	nitrate reductase	integral membrane	carbon starvation	NADH2 dehydrogenas	NADH2 dehydrogenas	hypothetical prote	putrescine-ornithi	mechanosensitive c	mechanosensitive c	probable membrane	probable amino aci	hypothetical prote	potassium transpor	hypothetical prote	hypothetical prote	О	hypothetical prote	Ψ	hypothetical prote		hypothetical prote	probable transmemb	hypothetical prote	transporter PAB217	•~	adenylyl cyclase t
ID	T13747	T19654	C88456	E69312	AI0561	E72523	S43882	S16447	D96506	F71651	F90693	B85544	H64776	AE0801	T24487	T02479	E86194	C82503	859107	S19366	B64090	AE1706	G71019	T24333	AI0034	T42693	E75217	T23656	A46180
DB	~	~	~	7	~	7	~	Н	7	~	~	N	~	~	~	~	~	7	~	~	~							7	0
Length	246	271	547	332	1120	604	495	495	379	429	1120	1120	1120	473	373	712	614	400	492	528	440	443	495	599	428	757	430	844	1165
% Query Match	26.0	20.7	9.8	7.4	7.1	7.0	6.9	6.8	6.7	6.7	6.7	•	•		•	9.9	•	6.5	•	•	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.3
Score	361.5	288	120	103	98.5	97	96	94	93.5	•	93	93	93	92.5	91.5		90.5	90	06	90	89.5	89.5	89.5	•	88	83	88.5	88.5	88
Result No.		7	е	4	2	y	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hemolysin III (ypl GGDEF family prote metabolite transpo	hypothetical prote bicyclomycin resis bicyclomycin resis	probable polygacch glutathione-regula transporter homolo glverophosphoryl	hypotherical prote hypotherical prote hypotherical prote	bicyclomycin resis F22L4.12 protein - spermidine/putresc
E70114 D82181 B69803	T24675 B91013 D85857	C95975 C83496 C69757 AH1151	G72589 D89865 G75133	E64987 E86146 E81179
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233 429 482	396 396	435 613 400 583	373 373 389	396 703 295
666		9 9 9 9	0.0.0	6.2.2 6.2.2 6.2.2
87.5 87.5 87.5	87.5 87 87	87 86.5 86.5	86.5 86 86 86	86 85.5
30			4 4 4 2 1 2	4 4 4 6 4 0

## ALIGNMENTS

RESULT 1

**T13747** 

T13747	
hypothetical protein 22E5.9 - fruit fly (Drosophila melanogaster)	la melanogaster)
C;Species: Drosophila melanogaster	
C;Date: 13-Aug-1999 #sequence revision 13-Aug-1999 #text change 09-Jul-2004	9 #text change 09-Jul-2004
C; Accession: T13747	
R;Murphy, L.; Harris, D.; Barrell, B.	
submitted to the EMBL Data Library, April 1999	
A; Description: Sequencing the distal X chromosome of Drosophila melanogaster.	of Drosophila melanogaster.
A; Reference number: Z17668	
A; Accession: T13747	
A;Status: preliminary; translated from GB/EMBL/DDBJ	J. C.
A; Molecule type: DNA	
A; Residues: 1-246 <mur></mur>	
A; Cross-references: UNIPROT: 077262; EMBL: AL031765; NID: e1371523; PID: e1326055; PIDN: CAA	; NID:e1371523; PID:e1326055; PIDN:CAA
C;Genetics:	
A; Cross-references: FlyBase: FBgn0000667	
A;Introns: 22/2; 63/1; 192/2	•
A; Note: EG: 22E5.9	
C;Superfamily: Caenorhabditis elegans hypothetical protein C33A11.2	l protein C33A11.2

4 11 LPSALVIWTSAAFIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAVLCIAT Gapa 13; Query Match 26.0%; Score 361.5; DB 2; Length 246; Best Local Similarity 33.6%; Pred. No. 3.5e-24; Matches 78; Conservative 50; Mismatches 91; Indels 13.

71 IYVRYKQVHAL---SPB-ENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSGAV 126 99 g à ଚ

127 LTFGMGSLYMFVQTILSYQMQPKIHGKQVFWIRLLLVIWCGVSALSML---TCSSVLHSG 183 셤 g ઠે

184 NFGTDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYIRDFQKISL 235 187 ઠે 셤

## RESULT 2 T19654

Apportetical protein C33A11.2 - Caenorhabditis elegans Csenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Accession: T19654 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004 R;Gajadsty, S: R;Gajadsty, S: Submitted to the EMBL Data Library, August 1996 A;Reference number: Z19158 A;Reference number: Z19158

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                A;Molecule type: DNA
A;Residues: 1-271 <WIL>
A;Cross-references: UNIRROT:093319; EMBL:279597; PIDN:CAB01861.1; GSPDB:GN00028; CESP:C3
A;Experimental source: clone C33A11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein W03A5.2 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: C88456
R;Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMOIGCUIG FYDE: DNA
A;Residues: 1-547 <STO>
A;Residues: 1-547 <STO>
A;Notes references: GB:chr_III; PIDN:AAA50731.1; PID:g485161; GSPDB:GN00021; CESP:W03A5.
C;Genetics:
A;Gene: W03A5.2
A;Map position: 3
                                                                                                                                                                                                                                                                                                                                   74 RYKOVHALSP--EENVIIKLNKAGLVIGILSCLGLSIVANPOKTTLFAAHVSGAVLTFGM 131
                                                                                                                                                                                                                                                                                                                                                              132 GSLYMPVQTILSYQMQPKIHGKQVFWIRLLLVIW---CGVSALSM-LTCSSVLHSGNFGT 187
                                                                                                                                                                                                                                                                                                                                                                                                                             73
                                                                                                                                                                                                                                                                                      51 PEKCLFGAMLNIAAVLCIATIYVRYKQVHALSPEEN---VIIKLNKAGLVLGILSCLGLS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 IVANFOKTTLFAAHVSGAVLTFGMGSLYMFVQTILSYQMQPKIHGKQVFWIRLLLVIWCG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168 VSALSMLTCSSVLHSGNFGTDLEQKLHWNPE-DKGYVLHMITTAAFWSMSFSFFGFFLTY 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 ALVIWTSAAFIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAVLCIATIYV
                                                                                                                     A,Map position: X
A,Introns: 26/1; 117/3; 177/1; 208/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C33A11.2
                                                                                                                                                                                                                                               12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 DLEOKLHWNPE--DKGYVLHMITTAAEWSMSFSFFGFFLTYIRDFQKISL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DLPTPRPWSRRIYQPGYELHQISALAEWGCAISQIFFIQSFGPEFEDISL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56;
                                                                                                                                                                                           Query Match

20.7%; Score 288; DB 2; Length 271
Best Local Similarity 30.9%; Pred. No. 1e-17;
Matches 71; Conservative 43; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.6%; Score 120; DB 2; Length 547;
Conservative 46; Mismatches 100; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 AYERREMPERPELIRGCTGYNERVFESCDVSEDEDNTL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 IRDFOKISLR-VEANLHGLTLYDT---APCPINNERTRLL 262
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                      A; Gene: CESP: C33A11.2
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nitrate reductase gamma subunit homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: O5-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: B69312
R;KLenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodsor
Glodek, A.; Zhou, L.; Ovacheek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
A;Authorse Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S
A;Authorse Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
A;Accession: B69312
A;Accession: B69312
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-332 <KLE>
A;Cross-references: UNIPROT:029749; GB:AE001069; GB:AE000782; NID:g2689392; PIDN:AAB9073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Integral membrane protein AefA [imported] - Salmonella enterica subsp. enterica serovar C;Species: Salmonella enterica subsp. enterica serovar Typhi C;Species: Salmonella enterica subsp. enterica serovar Typhi C;Dete: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: Al0561 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 K;Parkhill, J; Dougan, G; James, K.D; Thomson, N.R.; Pickard, D; Wain, J; Churcher, th, T; Connerton, P; Cronin, A; Davis, P; Davies, R.M.; Dowd, L; White, N; Farrar, S.; Moule, S; OʻGaora, P. Nature 413, 848-852, 2001 M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 VIGILSCLGLSIVANFQKTTIFFA-HVSGAVLTFGMGSLYMFVQTILSYQMQPKIHGKQV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:: | : | | : | |:
234 FYVHPALASF----LLAXFPFSKLMHAGGVFFSPTRNMPNDNRARRHVNPWDPADVPLLA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36
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A;Accession: A10561
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1120 <PAR>
A;Creses references: GB:AL513382; PIDN:CAD04963.1; PID:g16501750; GSPDB:GN00176
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----PSALVIWTSAAFIFSYITAVTLHH----I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPALPYISDTGTVAPEKCLFGAMLNIAAVLCIATIYVRYKQVHALSPEENVIIKLNKAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 FWIRLLLVIWCGVSALSMLTCSSVLHSG------NFGTDLEQKLH---WNPEDKGYVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
7.4%; Score 103; DB 2; Length 332;
Best Local Similarity 17.0%; Pred. No. 0.18;
Matches 45; Conservative 47; Mismatches 112; Indels
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7.1%; Score 98.5; DB 2; Length 11
Best Local Similarity 19.5%; Pred. No. 1.6;
Matches 58; Conservative 46; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 HMITTAA-----EWSMSFSFF 220
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Mol. Gen. Genet. 243, 97-105, 1994
A/Title: Intron 1088 from the NADH dehydrogenase subunit 4 gene of lettuce mitochondria
A/Reference number: S43882; MUID:94247363; PMID:8190077
A/Accession: S43882
A/Status: preliminary
A/Status: preliminary
A/Residues: 1-495 <GEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NaDH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain 4 - wheat mitochondrion NiAlternate names: mitochondrial complex I subunit IV (Species mitochondrion Triticum aestivum (common wheat) (Species mitochondrion 10-Sep-1999 #text_change 09-Jul-2004 (Species mitochondrion 10-Sep-1999 #text_change 09-Jul-2004 M: Archamatina, L.; Grienenberger, J.M.

Nucleic Acids Res. 19, 3275-3282, 1991 A; Title: RNA editing of the transcript coding for subunit 4 of NADH dehydrogenase in wh A; Reference number: 816447; MUID:91288205; PMID:1712098 A; Molecule type: mRNA A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-14, P. 16-24, TP', 27-35, P', 37-51, PP', 54, PR', 57-65, S', 67-105, S', 107-1
A; Residues: 1-14, P', 479-495 <LAE>
A; Residues: 1-14, P', 479-495 <LAE>
A; Cross-references: EMBL:X7164; NID:g21823; PIDN:CAA40453.1; PID:g21824
A; Note: the authors translated the codon CGT for residue 418 as Ala
A; Note: 15-P, 25-Thr, 26-Pro, 36-Pro, 52-Pro, 55-Pro, 56-Arg, 66-Ser, 106-Ser, re due to RNA editing.
R; Lamattina, L.; Well, J.H.; Grienenberger, J.M.
R; Lamattina, L.; Pell, 79-83, 1989
A; Title: RNA editing at a splicing site of NADH dehydrogenase subunit IV gene transcrip
A; Reference number: S06835; MUID:90076495; PMID:2687023
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A;Introns: 154/2; 326/1; 467/1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                   A;COSETECETEDCES: UNIPROT:Q37544
A;Crostfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          392 PGTSSFIGEFLILVGAFQRNSLVATLAALGMILGAAYSLWLY-NRVVSGNLKPDFLHKFS 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 GGSILLMLSHGLVSSALFLCVGVLYVRHKTRLVRYYGGLVSTMPNFSTIFFFFTLANMSL 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               277 LCFTP----FIYTLSAIAIIYTSLTTLRQID--LKKLIAYSSVAHMNLVTIGMFSLNIQGI 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 LSFLPSALVIWISAAFIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAM--LNI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------AAVLCIATIYVRYKQ------VHALSPBENVIIKLNKAGLVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 -GILSCLG--LSIVANFOKTTLFAAHVSGAVLTFGMGSLYMFVQTILSYQMQP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 495;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 KIHGKOVF-WIRLLL-VIWCGVSALSMLTC----SSVLHSGNF 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
6.9%; Score 96; DB 2
Best Local Similarity 24.6%; Pred. No. 1.1;
Matches 55; Conservative 34; Mismatches
R;Geiss, K.T.; Abbas, G.M.; Makaroff, C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: S06835
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R; Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah awa, H.; Takamyaya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Vamazaki, J.; K DN Res. 6, 83-101, 1999
A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A; Reference number: A72450; MUID:99310339; FMID:10382966
A; Reference number: A72450; MUID:99310339; FMID:10382966
A; Reference presion: E72523
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-604 cKAW>
A; Coss-references: UNIPROT:Q9Y9X7; DDBJ:AP000063; NID:g5105654; PIDN:BAA81173.1; PID:g5
A; Experimental source: strain K1
C; Genetics:
C; Superfamily: carbon starvation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carbon starvation protein A homolog APE2162 [similarity] - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NADH2 dehydrogenase (ubiguinone) (EC 1.6.5.3) chain 4 - garden lettuce mitochondrion C;Species: mitochondrion Lactuca sativa (garden lettuce) C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004 C;Accession: S43882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                           -----NIAAVLCIATIYVRYKQVHALSPEBNVIJKLNKAGLVLGILS- 102
                                                                                                                                                                                                                                                                                              GMGSLYMF 137
                                                                                                                                                                                                                                                                                                                                                                                                                                              VQTILSYQMQPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSG-NFGTDLEQKLHWN 196
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                                                                                                                                                                                                                                                                                                                                                                    SWDKLQWLAAALSVGLGFGLQEIFGNFVSGLIILFERPVRIGDTVTIGTYSGTVSKIRIR 967
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                                                                     ----AIWSDLITVFSYLDSITLWHYNG----SEAGAAVVKSVTMGSLL
                                                                                                                                                                                         848 FAIIAAMVAWALIRNLPGLLEVLVLSRLNMRQGASYAITTILNYVIIAVGAMTVFGSLGV
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MWWFQQGLSFLPSALVIWTSAAFIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML
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                                                                                                                                                                                                                                                                                          -----CLGLSIVANFQKTTLFAAHVSGAVLTF-
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Matches 69; Conserv
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C;Accession: F71651
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U A;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71651
A;Reference number: A71650; MUID:99039499; PMID:9823893
A;Reference number: A71651
A;Rostus: preliminary; nucleic acid sequence not shown; translation not shown A;Rosidues: 1-429 <AND>A;Rosidues: 1-429 <AND>A;Rosidues: 1-429 <AND>A;Rosidues: 1-429 <AND>A;Rosidues: 1-429 <AND>A;Coss-references: UNIPROT:092D63; GB:AJ235272; GB:AJ235269; NID:g3861033; PIDN:CAA1493|C;Genetics: A;Gene: pock: RP483
C;Superfamily: L-Lysine transport protein
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                                                                11;
                                                                                                                                             277 LCFTP---FIYTLSAIAIIYTSLTTLRQID--LKKİTAYSSVAHMMLVTIGMFSLNİQGI 331
                                                                                                                                                                                                                                                            332 GGSILLMLSHGLVSSÅLFLCVGVLYDRHKTRLVRYYGGLVSTMPNFSTIFFFFTLÅNMSL 391
                                                                                                                                                                                                                                                                                                                          99 -GILSCLG--LSIVANPOKTTLFAAHVSGAVLTFGMGSLYMFVOTILSYQMQP----- 148
                                                                                                                                                                                                                                                                                                                                                                  392 PGTSSFIGEFLILVGAFQRNSLVATLRALGMILGAAVSLMLY-NRVVSGNLKFDFLYKFS 450
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                                                                                                                                                                                                           63 ------VHALSPEENVIIKIAKG------VHALSPEENVIIKLAKAGLVL
                                                                Gaps
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                                                             52;
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A/Map position: 1
C/Superfamily: Arabidopsis thaliana hypothetical protein T9A21.70
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                                                       84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            KIHGKQVFWIR--LLLVIWCGVSALSMLTC----SSVLHSGNF 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DINGREVELFLPPLYGVVWMGVYPKVFLDCMHTSVSNLVQHGKF 494
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1 Similarity 21.8%; Pred. No. 1.4;
47; Conservative 53; Mismatches
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Best Local Similarity
Matches 47; Conserv
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Mechanosensitive channel protein [imported] - Escherichia coli (strain O157:H7, substrail C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 18-Unl-2001
C;Accession: F90693
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Hite: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F90693
A;Molecule type: DNA
A;Residues: 1-1120 cHAY>
A;Residues: 1-1120 cHAY>
A;Escidues: 1-1120 cHAY>
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                          217 IPRAIIIGTCCVAFLXIINSIGIIGLIPASELINSKAPY-ADAATL----LFGGTWSKV 270
                                                                                                                                                                                     62 ---IAAVLCIATI---YVRYKQVHALSPEBNVIIKL-----NKAGLVLGILSCLGLSIV 109
                                                                                                                                                                                                                   271 ITVIASVICIGTLNAWVLTSGQIALGLABDGLLFKFFAKKNSNAPTYGIIISCLGITPL 330
                                                                                                                                                                                                                                                                              110 ANFOKTTLFRAAHVSGAVLTFGMGSLYMFVQTILSYQMQPKI-HGKQVFWIRLLLVIWCGV 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --- GMGSLYMF 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                             11 LPSALVIWTSAAFIFSYITAVTLHHIDPA-----LPYISDTGTVAPEKCLFGAMLN--
                                                                                                                                                                                                                                                                                                              331 LLFTSNNNFAKQIT-QIIDFSV-IAFLFVYLICSLAFLKVIFSSKENFSYYYLF----V
                                                           79; Indels 35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MWWFQQGLSFLPSALVIWTSAAFIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ------INIAAVLCIATIYVRYKQVHALSPERNVIIKLNKAGLVLGILS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 VQTILSYQMQPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSG-NFGTDLEQ 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99
                      Length 429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 1120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 -----CLGLSIVANFOKTTLFAAHVSGAVLTF-----
                   DB 2;
Query Match
6.7%; Score 93.5; Di
Best Local Similarity 24.1%; Pred. No. 1.6;
Matches 48; Conservative 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.7%; Score 93; DB;
Best Local Similarity 19.6%; Pred. No. 5;
Matches 46; Conservative 38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    384 AIISIIFCTWVIYKTPFET 402
                                                                                                                                                                                                                                                                                                                                                                         SALSMLTCSSVLHSGNFGT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
A;Gene: ECs0518
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putrescine-ornithine antiporter (potB) RP483 - Rickettsia prowazekii C;Species: Rickettsia prowazekii C;Date: 21-Nov-1998 #sequence\_revision 21-Nov-1998 #text\_change 09-Jul-2004

F71651

-----GMGSLYMF 137

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848 FAIIASMVAWALIRNLPGLLEVLVLSRLNMRQGASYAITTILNYIIIAVGAMTVFGSLGV 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           908 SWDKLQWLAAALSVGLGFGLQEIFGNFVSGLILLFERPVRIGDTVTIGSFSGTVSKIRIR 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GB: AL513382; PIDN: CAD07591.1; PID: g16503583; GSPDB: GN00176 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 --FGMGSLYMF-VQTILSYQMQPKIHGKQVFWIRLL--LVIWCGV---SALSMLTCSSVL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 AFIGIGSAVIFWLLTLMN-----IRGME--WTKIINSISAWCGVFIPSAILLLLAVVWL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 ------GYMIGGGLAENK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 SALVIWTSAAFIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAVLCIATIY 72
                                                                                                                                                                                                                                                                                                                                    61 -------NIAAVLCIATIYVRYKQVHALSPERNVIIKLNKAGLVLGILS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 VRYKQVHALSPEENVIIKLNKAGLVLGILSC-LGLSIVANPQKTTLFAAHVSGAVLT---
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                                                                                                                                                                                                   1 MWWFQQGLSFLPSALVIWISAAFIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTITDFDRKEVIIPNKAF-VTERLINW----SLTDTTTRLVIRLGVAYGSDLEK 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 VQTILSYQMQPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSG-NFGTDLEQ 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.6%; Score 92.5; DB 2; Length 47
Best Local Similarity 22.8%; Pred. No. 2.1;
Matches 59; Conservative 36; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----CLGLSIVANFQKTTLFAAHVSGAVLTF-----
7;892-908/Domain: transmembrane #status predicted <TM9>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
T24487
hypothetical protein T05Al.1 - Caenorhabditis elegans
                                                                                                                                    38; Mismatches
                                                              Score 93;
Pred. No.
                                                              Query Match
Best Local Similarity 19.6%;
Matches 46; Conservative 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: STY2589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103
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A.Status: nucleic acid sequence not shown; translation not shown
A.Molecule type: DNA
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-1120 < BLAT>
A.Cross-references: UNIPROT:P77338; GB:AE000152; GB:U00096; NID:g1786660; PIDN:AAC73567.
A.Experimental source: strain K-12, substrain MG1655
C.Genetics:
A.Gene: aefA
C.Keywords: transmembrane #status predicted <TM1>
F.12-28/Domain: transmembrane #status predicted <TM2>
F.504-520/Domain: transmembrane #status predicted <TM4>
F.561-577/Domain: transmembrane #status predicted <TM4>
F.630-666/Domain: transmembrane #status predicted <TM5>
F.630-660/Domain: transmembrane #status predicted <TM6>
F.631-679/Domain: transmembrane #status predicted <TM6>
F.631-679/Domain: transmembrane #status predicted <TM6>
F.644-860/Domain: transmembrane #status predicted <TM6>
F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-860/F.644-86
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R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, N.T.tle: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.

A; Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.

A; Reference number: A85480; MUID:21074935; PMID:11206551

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-1120 < STO>

A; Cross-references: UNIPROT: Q8XD54; GB: AE005174; NID:g12513332; PIDN: AAG54814.1; GSPDB: G

A; Genetics:
A; Genetics: atrain O157:H7, substrain EDL933
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                                                                                                                                                                                               mechanosensitive channel protein [similarity] - Escherichia coli (strain 0157:H7, substx
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C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Accession: H64776
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------NIAAVLCIATIYVRYKQVHALSPEENVIIKLNKAGLVLGILS- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            908 SWDKLQWLAAALSVGLGFGLQEIFGNFVSGLIILFERPVRIGDTVTIGSFSGTVSKIRIR 967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MWWFQQGLSFLPSALVIWTSAAFIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
                                                                                                                                                                                                                                  Species: Escherichia coli
Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
968 ATTITDFDRKEVIIPNKAF-VTERLINW----SLTDTTRLVIRLGVAYGSDLEK 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 1120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.7%; Score 93; DB 2
Best Local Similarity 19.6%; Pred. No. 5;
Matches 46; Conservative 38; Mismatches
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
R;Lloyd, C.
Submitted to the EMBL Data Library, December 1995
A;Reference number: Z19897
A;Reference number: Z19897
A;Accession: T24487
A;Accession: T24487
A;Accession: T24487
A;Accession: UNIPROT:Q22188; EMBL:Z68219; PIDN:CAA92481.1; GSPDB:GN00022; CESP:TdAspecial Fype: DNA
A;Residues: 1-373 <WIL->
A;Coss-references: UNIPROT:Q22188; EMBL:Z68219; PIDN:CAA92481.1; GSPDB:GN00022; CESP:TdAspecial: Sizerinental Source: clone T05A1
A;Experimental Source: clone T05A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 ATIYVRYKQVHALSPBENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAH----- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 VSGA---VLIFGMGSLYMFVQTILSYQMQPKIHGKQVFWIRLLLVIWCGVSALSMLTCSS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 VLHSGNFGTDLE-OKL-----HWNPED--KGYVLHMITTAABWSMSFSFFFFLT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 -----YGWYMDVEKLNGLCGEYCSEHWPLAEVRKGYTFLVLIT----QFLFFPFATMAFC 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.6%; Score 91.5; DB 2; Length 373;
Best Local Similarity 23.0%; Pred. No. 2;
Matches 50; Conservative 34; Mismatches 82; Indels 51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 YIRDFQKISLRVEANLHGLTLYDTAPCPINNERTRLL 262
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------SERSQLL 234
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